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Notes on Phylogenetic Relationships of the Tribe Phrissomini (Coleoptera, Cerambycidae) Inferred from Mitochondrial COI Gene Sequences

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The tribe Phrissomini THOMSON, 1860 consists of flightless longicorn beetles with atrophied hindwings. Three genera, including the following six species of this tribe are distributed in and endemic to Japan, *Hayashiechthistatus inexpectus* (HAYASHI), *Parechthistatus gibber* (BATES), *Mesechthistatus binodosus* (WATERHOUSE), *M. furciferus* (BATES), *M. taniguchii* (SEKI) and *M. fujisanus* HAYASHI. Molecular phylogenetic approach is a method of utility to investigate the phylogenetic relationships at inter-taxon level and chronological distance of divergence. We have already reported molecular analyses on phylogeny, both intergeneric one [for *Parechthistatus gibber* and *Hayashiechthistatus inexpectus* (NAKAMINE & TAKEDA, 2008 a)] and intrageneric one [for four *Mesechthistatus* species (NAKAMINE & TAKEDA, 2008 b)]. However, we have not published our results of molecular phylogenetic analysis at intra-tribe level. Here we provide the phylogenetic relationships by the analysis that was carried out based on partial sequences from the mitochondrial cytochrome oxidase subunit I (COI) gene from six different species of tribe Phrissomini.

Materials and Methods. The analytical methods are the same as already described by NAKAMINE & TAKEDA (2008 a, 2008 b). Two lamiine species, *Plectrura metallica yoshihiroi* TAKAKUWA and *Dolichoprosopus yokoyamai* (GRESSITT) were used as outgroup.

Results and discussion. Figure 1 shows the maximum likelihood tree of the mitochondrial

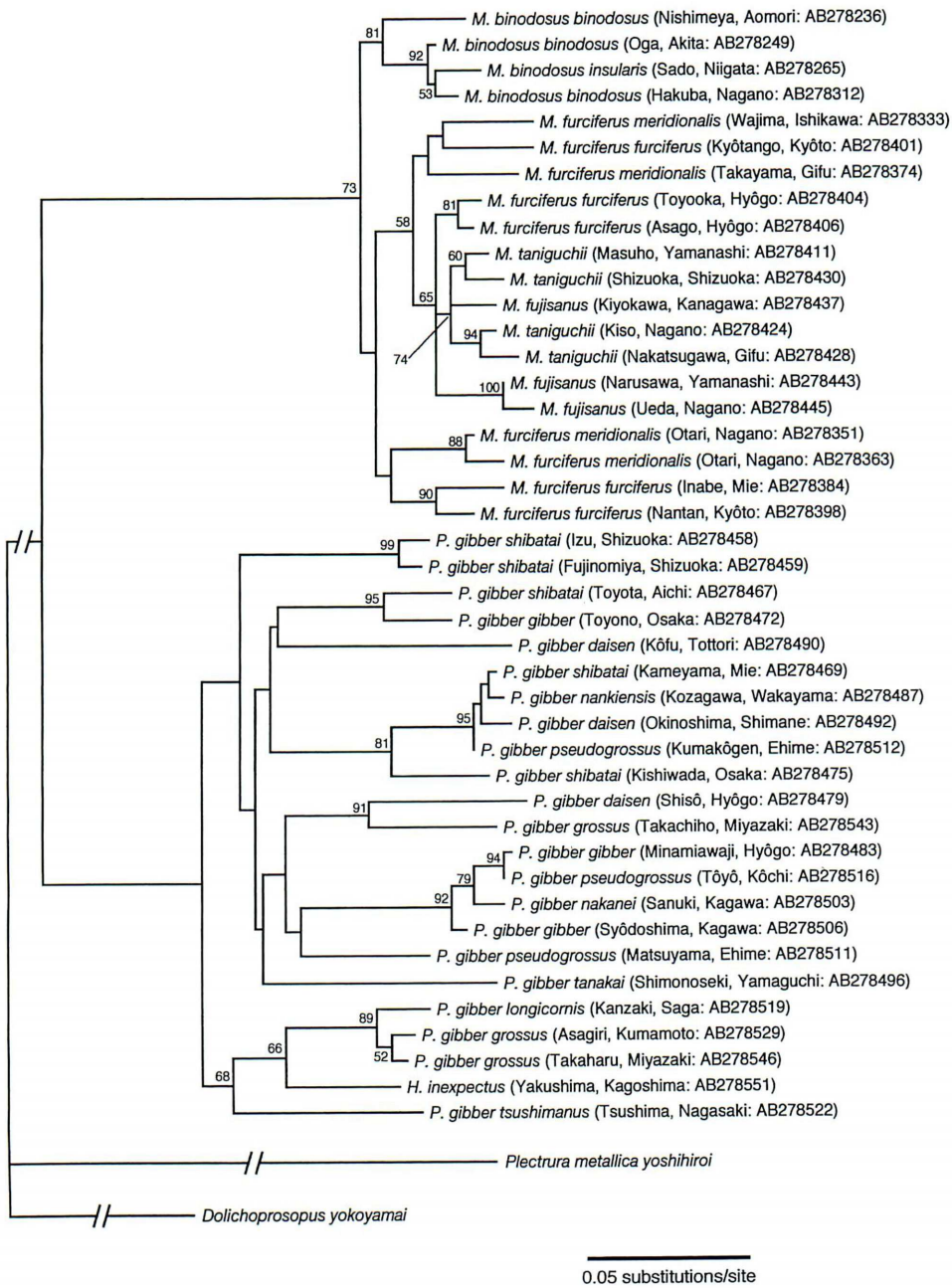

Fig. 1. A maximum likelihood phylogenetic tree based on the mitochondrial COI gene sequences of the Phrissomini. The bootstrap value is indicated at each node (when $>50\%$). The accession number for DDBJ, EMBL and GenBank is indicated after locality where the sample was collected. Note. Since the outgroup branch was too long, it was omitted.

COI gene of the tribe Phrissomini. The average branch length at ancestral node to tips is 0.082 in *Parechthistatus/Hayashiechthistatus* lineage and ditto branch length is 0.041 in *Mesechthistatus* lineage. This results suggest that the mitochondrial COI gene haplotypes of *Parechthistatus/Hayashiechthistatus* lineage diverged in an older age than the radiation of *Mesechthistatus* lineage.

The estimation of the divergence date based on DNA sequence data is one of the major aims for molecular phylogenetic analyses. The evolutionary rate of the COI gene has already been estimated in other insects, and the values range from 1.5% to 2.3% per 1 million years (see details BROWER, 1994; FARRELL, 2001; QUEK *et al.*, 2004; SOTA & HAYASHI, 2007). These values were used to estimate the date of divergence to *Parechthistatus/Hayashiechthistatus* lineage and *Mesechthistatus* lineage in this report. The average value for genetic divergence between *Parechthistatus/Hayashiechthistatus* and *Mesechthistatus* was 9.68±0.62 (mean±SD) %. Application of the estimated values for the evolutionary rate of the COI gene (1.5% to 2.3%) dated the divergence of *Parechthistatus/Hayashiechthistatus* and *Mesechthistatus* between 6.45 and 4.2 million years ago. This suggests that *Parechthistatus/Hayashiechthistatus* and *Mesechthistatus* diverged at the end of the Miocene epoch through the early Pliocene epoch in the Tertiary era.

Figure 1 shows that *Hayashiechthistatus inexpectus* was included in the *Parechthistatus* lineage. This result suggests the possibility that *H. inexpectus* has speciated from *P. gibber*. However, there is a possibility that original mtDNA haplotype of *H. inexpectus* has been extinguished by introgressive hybridization between *P. gibber* population and *H. inexpectus* (NAKAMINE & TAKEDA, 2008 a).

In Figure 1, *M. binodosus* is shown as monophyletic. However, *M. furciferus*, *M. taniguchii*, and *M. fujisanus* are not monophyletic, forming instead a complex. These results suggest that it was caused by introgressive hybridization or lineage sorting of ancestral polymorphism (NAKAMINE & TAKEDA, 2008 b).

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